

Patent Application US/07/800,364

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Hewick, Rodney M.

Wang, Jack H.

Wozney, John M.

Celeste, Anthony J.

(ii) TITLE OF INVENTION: Bone and Cartilage Inductive Proteins

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Legal Affairs, Genetics Institute, Inc.

(B) STREET: 87 CambridgePark Drive

(C) CITY: Cambridge

(D) STATE: MA

(E) COUNTRY: USA

(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kapinos, Ellen J.

(B) REGISTRATION NUMBER: 32,245

(C) REFERENCE/DOCKET NUMBER: GI 5182A

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

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54 (iii) HYPOTHETICAL: NO
55
56 (iv) ANTI-SENSE: NO
57
58 (vi) ORIGINAL SOURCE:
59 (F) TISSUE TYPE: Bone
60
61
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
63
64 Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu Asp Trp
65 1 5 10 15
66
67 Val Ile Ala Pro Gln Gly Tyr
68 20
69
70 (2) INFORMATION FOR SEQ ID NO:2:
71
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 18 amino acids
74 (B) TYPE: amino acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: unknown
77
78 (ii) MOLECULE TYPE: peptide
79
80 (iii) HYPOTHETICAL: NO
81
82 (iv) ANTI-SENSE: NO
83
84 (v) FRAGMENT TYPE: internal
85
86 (vi) ORIGINAL SOURCE:
87 (A) ORGANISM: Bos taurus
88 (F) TISSUE TYPE: Bone
89
90
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
92
93 Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile
94 1 5 10 15
95
96 Leu Arg
97
98
99 (2) INFORMATION FOR SEQ ID NO:3:
100
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 7 amino acids
103 (B) TYPE: amino acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: unknown
106

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107 (ii) MOLECULE TYPE: peptide
108
109 (iii) HYPOTHETICAL: NO
110
111 (iv) ANTI-SENSE: NO
112
113 (vi) ORIGINAL SOURCE:
114 (A) ORGANISM: Bos taurus
115 (F) TISSUE TYPE: Bone
116
117
118 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
119
120 Ala Cys Cys Ala Pro Thr Lys
121 1 5
122
123 (2) INFORMATION FOR SEQ ID NO:4:
124
125 (i) SEQUENCE CHARACTERISTICS:
126 (A) LENGTH: 23 amino acids
127 (B) TYPE: amino acid
128 (C) STRANDEDNESS: single
129 (D) TOPOLOGY: unknown
130
131 (ii) MOLECULE TYPE: peptide
132
133 (iii) HYPOTHETICAL: NO
134
135 (vi) ORIGINAL SOURCE:
136 (A) ORGANISM: Bos taurus
137 (F) TISSUE TYPE: Bone
138
139
140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
141
142 Thr Asn Glu Leu Pro Pro Pro Asn Lys Leu Pro Gly Ile Phe Asp Asp
143 1 5 10 15
144
145 Val His Gly Ser His Gly Arg
146 20
147
148 (2) INFORMATION FOR SEQ ID NO:5:
149
150 (i) SEQUENCE CHARACTERISTICS:
151 (A) LENGTH: 80 base pairs
152 (B) TYPE: nucleic acid
153 (C) STRANDEDNESS: double
154 (D) TOPOLOGY: linear
155
156 (ii) MOLECULE TYPE: DNA (genomic)
157
158 (iii) HYPOTHETICAL: NO
159

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160 (iv) ANTI-SENSE: NO
161
162 (vi) ORIGINAL SOURCE:
163 (A) ORGANISM: Bos taurus
164
165 (vii) IMMEDIATE SOURCE:
166 (B) CLONE: acc30
167
168 (viii) POSITION IN GENOME:
169 (C) UNITS: bp
170
171 (ix) FEATURE:
172 (A) NAME/KEY: CDS
173 (B) LOCATION: 25..57
174
175
176 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
177
178 GGATCCGCGT GCTGTGCTCC GACC AAG CTG AGC GCC ACC TCC GTG CTC TAC 51
179 Lys Leu Ser Ala Thr Ser Val Leu Tyr
180 1 5
181
182 TAC GAC AGCAGCAACA ATGTAATTCT AGA 80
183 Tyr Asp
184 10
185
186
187 (2) INFORMATION FOR SEQ ID NO:6:
188
189 (i) SEQUENCE CHARACTERISTICS:
190 (A) LENGTH: 11 amino acids
191 (B) TYPE: amino acid
192 (D) TOPOLOGY: linear
193
194 (ii) MOLECULE TYPE: protein
195
196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
197
198 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
199 1 5 10
200
201 (2) INFORMATION FOR SEQ ID NO:7:
202
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 199 base pairs
205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: double
207 (D) TOPOLOGY: linear
208
209 (ii) MOLECULE TYPE: DNA (genomic)
210
211 (iii) HYPOTHETICAL: NO
212

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213 (vi) ORIGINAL SOURCE:
214 (A) ORGANISM: Bos Taurus
215
216 (vii) IMMEDIATE SOURCE:
217 (A) LIBRARY: Bovine genomic
218 (B) CLONE: Lambda 9800-10
219

220 (viii) POSITION IN GENOME:
221 (C) UNITS: bp
222

223 (ix) FEATURE:
224 (A) NAME/KEY: exon
225 (B) LOCATION: 30..199
226

227 (ix) FEATURE:
228 (A) NAME/KEY: intron
229 (B) LOCATION: 1..29
230

231 (ix) FEATURE:
232 (A) NAME/KEY: CDS
233 (B) LOCATION: 30..179
234
235

236 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
237

238 TGCCCGCTGC CCCCTCCCGC CCCC GCCAG GTG CAC CTG CTG AAG CCG CAC GCG 53
239 Val His Leu Leu Lys Pro His Ala
240 1 5
241

242 GTC CCC AAG GCG TGC TGC GCG CCC ACC AAG CTG AGC GCC ACT TCC GTG 101
243 Val Pro Lys Ala Cys Cys Ala Pro Thr Lys Leu Ser Ala Thr Ser Val
244 10 15 20
245

246 CTC TAC TAC GAC AGC AGC AAC AAC GTC ATC CTG CGC AAG CAC CGC AAC 149
247 Leu Tyr Tyr Asp Ser Ser Asn Asn Val Ile Leu Arg Lys His Arg Asn
248 25 30 35 40
249

250 ATG GTG GTC CGC GCC TGC GGC TGC CAC TGAGGCCCA ACTCCACCGG 196
251 Met Val Val Arg Ala Cys Gly Cys His
252 45 50
253

254 CAG 199
255
256

257 (2) INFORMATION FOR SEQ ID NO:8:
258

259 (i) SEQUENCE CHARACTERISTICS:
260 (A) LENGTH: 49 amino acids
261 (B) TYPE: amino acid
262 (D) TOPOLOGY: linear
263

264 (ii) MOLECULE TYPE: protein
265

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266 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

267
268 Val His Leu Leu Lys Pro His Ala Val Pro Lys Ala Cys Cys Ala Pro
269 1 5 10 15
270
271 Thr Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp Ser Ser Asn Asn
272 20 25 30
273
274 Val Ile Leu Arg Lys His Arg Asn Met Val Val Arg Ala Cys Gly Cys
275 35 40 45
276
277 His
278
279
280

281 (2) INFORMATION FOR SEQ ID NO:9:

282

283 (i) SEQUENCE CHARACTERISTICS:

284 (A) LENGTH: 172 base pairs

285 (B) TYPE: nucleic acid

286 (C) STRANDEDNESS: double

287 (D) TOPOLOGY: linear

288

289 (ii) MOLECULE TYPE: DNA (genomic)

290

291 (iii) HYPOTHETICAL: NO

292

293 (vi) ORIGINAL SOURCE:

294 (A) ORGANISM: Bos taurus

295

296 (vii) IMMEDIATE SOURCE:

297 (A) LIBRARY: Bovine genomic

298 (B) CLONE: Lambda 9800-10

299

300 (viii) POSITION IN GENOME:

301 (C) UNITS: bp

302

303 (ix) FEATURE:

304 (A) NAME/KEY: exon

305 (B) LOCATION: 51..161

306

307 (ix) FEATURE:

308 (A) NAME/KEY: intron

309 (B) LOCATION: 1..50

310

311 (ix) FEATURE:

312 (A) NAME/KEY: intron

313 (B) LOCATION: 162..172

314

315 (ix) FEATURE:

316 (A) NAME/KEY: CDS

317 (B) LOCATION: 51..161

318

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319
320 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
321
322 GGGGTGGGAG GGCACGTGGA TGGGACTCAC CTTCTCCAC TACCCCCCAG GAC TGG 56
323 Asp Trp
324 1
325
326 GTC ATC GCC CCC CAA GGC TAC TCA GCC TAT TAC TGT GAA GGG GAG TGC 104
327 Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly Glu Cys
328 5 10 15
329
330 TCC TTC CCG CTG GAC TCC TGC ATG AAC GCC ACC AAC CAC GCC ATC CTG 152
331 Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala Ile Leu
332 20 25 30
333
334 CAG TCC CTG GTCAGTACCT C 172
335 Gln Ser Leu
336 35
337
338
339 (2) INFORMATION FOR SEQ ID NO:10:
340
341 (i) SEQUENCE CHARACTERISTICS:
342 (A) LENGTH: 37 amino acids
343 (B) TYPE: amino acid
344 (D) TOPOLOGY: linear
345
346 (ii) MOLECULE TYPE: protein
347
348 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
349
350 Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser Ala Tyr Tyr Cys Glu Gly
351 1 5 10 15
352
353 Glu Cys Ser Phe Pro Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
354 20 25 30
355
356 Ile Leu Gln Ser Leu
357 35
358
359 (2) INFORMATION FOR SEQ ID NO:11:
360
361 (i) SEQUENCE CHARACTERISTICS:
362 (A) LENGTH: 119 base pairs
363 (B) TYPE: nucleic acid
364 (C) STRANDEDNESS: double
365 (D) TOPOLOGY: linear
366
367 (ii) MOLECULE TYPE: DNA (genomic)
368
369 (iii) HYPOTHETICAL: NO
370
371 (vi) ORIGINAL SOURCE:

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372 (A) ORGANISM: Bos taurus

373

374 (vii) IMMEDIATE SOURCE:

375 (A) LIBRARY: Bovine genous

376 (B) CLONE: Lambda 9800-10

377

378 (viii) POSITION IN GENOME:

379 (C) UNITS: bp

380

381 (ix) FEATURE:

382 (A) NAME/KEY: exon

383 (B) LOCATION: 20..99

384

385 (ix) FEATURE:

386 (A) NAME/KEY: intron

387 (B) LOCATION: 1..19

388

389 (ix) FEATURE:

390 (A) NAME/KEY: intron

391 (B) LOCATION: 100..119

392

393 (ix) FEATURE:

394 (A) NAME/KEY: CDS

395 (B) LOCATION: 22..99

396

397

398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

399

400 CCCTTGCGTG TCCCCGCAGA C GAC GTC CAC GGC TCC CAC GGC CGG CAG GTG 51

401 Asp Val His Gly Ser His Gly Arg Gln Val

402 1 5 10

403

404 TGC CGT CGG CAC GAG CTG TAC GTG AGC TTC CAG GAC CTG GGC TGG CTG 99

405 Cys Arg Arg His Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu

406 15 20 25

407

408 GTGAGTTCCG ACTCTCCTTT 119

409

410

411 (2) INFORMATION FOR SEQ ID NO:12:

412

413 (i) SEQUENCE CHARACTERISTICS:

414 (A) LENGTH: 26 amino acids

415 (B) TYPE: amino acid

416 (D) TOPOLOGY: linear

417

418 (ii) MOLECULE TYPE: protein

419

420 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

421

422 Asp Val His Gly Ser His Gly Arg Gln Val Cys Arg Arg His Glu Leu

423 1 5 10 15

424

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425 Tyr Val Ser Phe Gln Asp Leu Gly Trp Leu
426 20 25

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

LINE ERROR

ORIGINAL TEXT

30 Wrong application Serial Number

(A) APPLICATION NUMBER: US

PAGE: 1

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA
APPLICATION NUMBER
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/07/800,364

DATE: 12/16/91
TIME: 12:00:44

LINE ORIGINAL TEXT

CORRECTED TEXT

BACKUP/RESTORE TRANSACTION

Transaction Number:

3383

12/16/91

START TIME: 11:49:13

END TIME: 12:01:11

PROCESSING TIME: 0:11:58

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|---------------------------|---|---------------|
| Translog Code | : | DOSCOPY |
| Application Serial Number | : | US/07/800,364 |
| National PCT | : | N |
| Admendment | : | |
| Application Class | : | 514 |
| Application File Dt. | : | 19911126 |